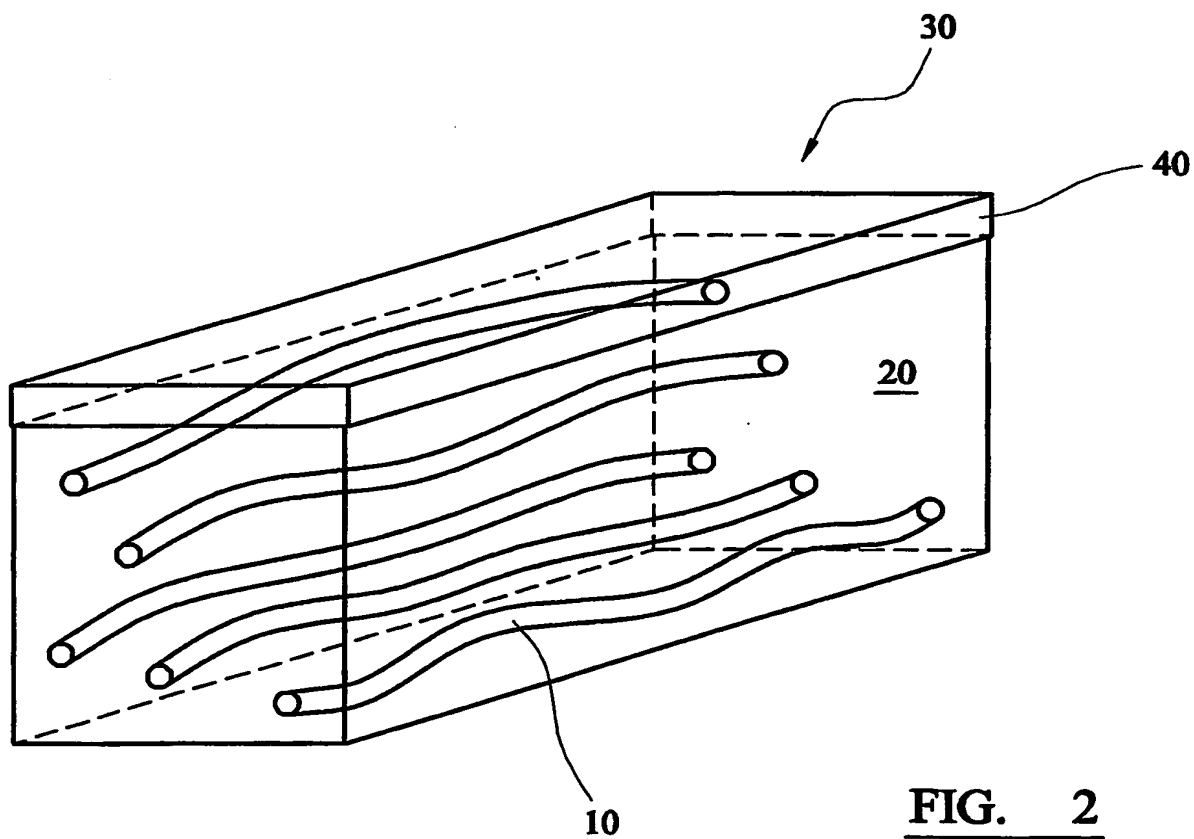
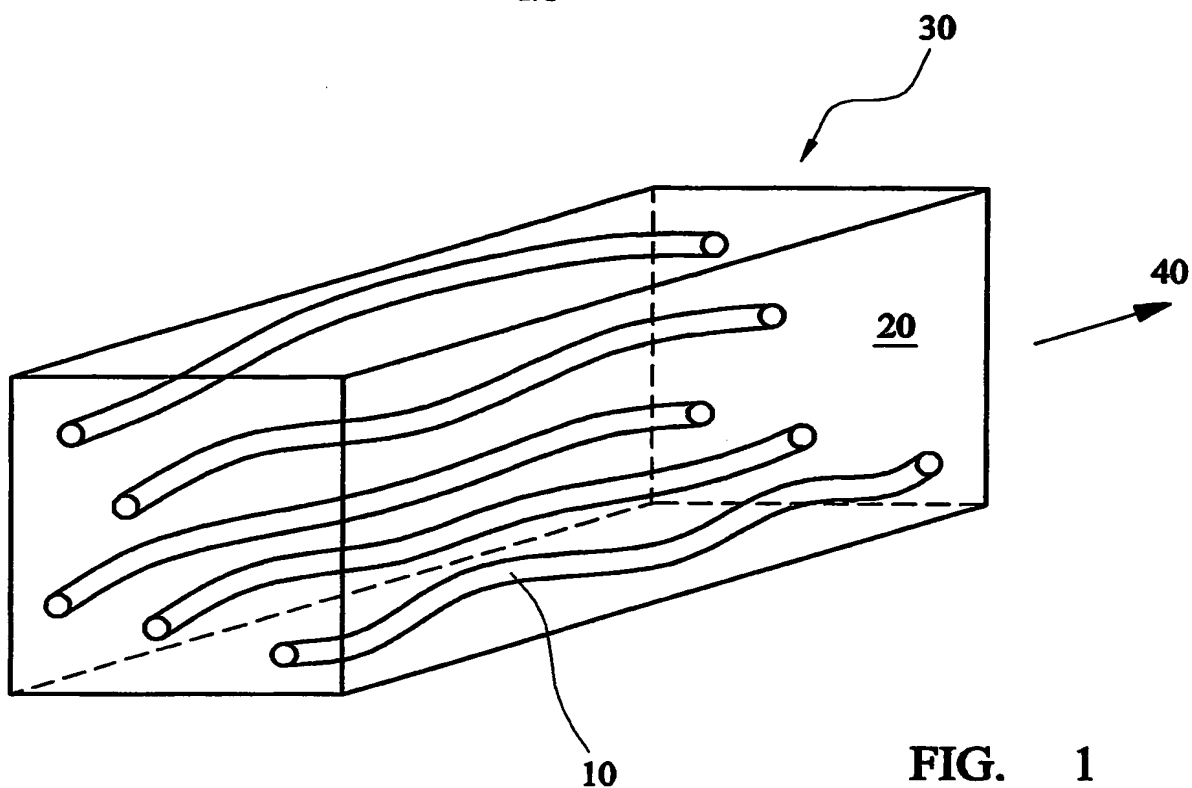


-1/5-



-2/5-

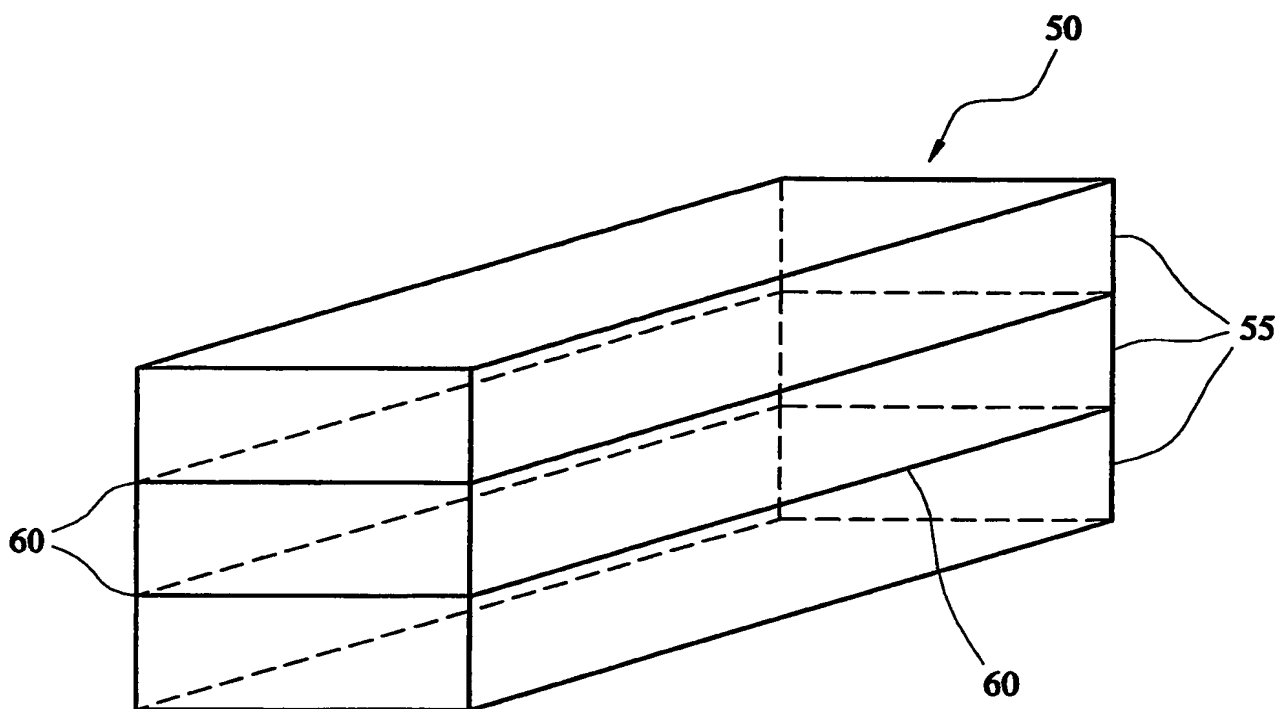


FIG. 3

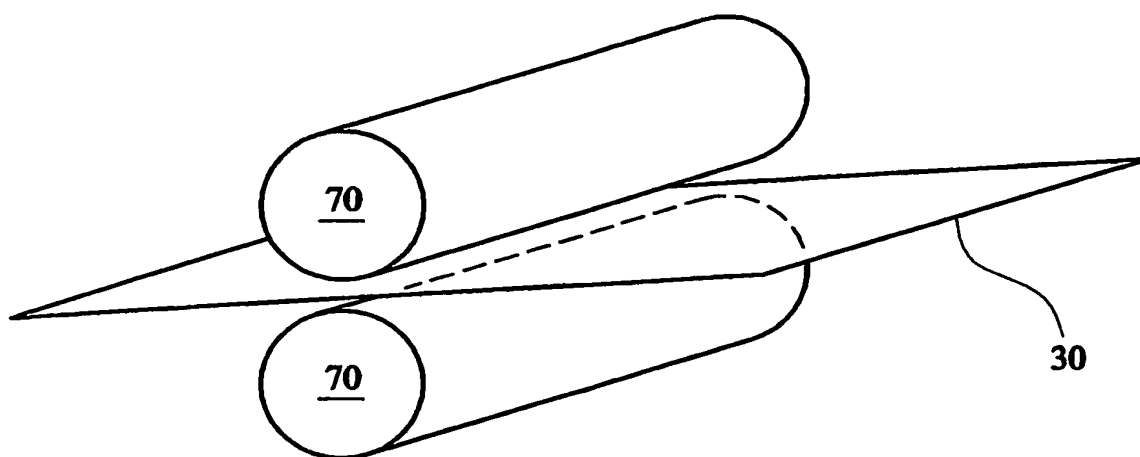


FIG. 4

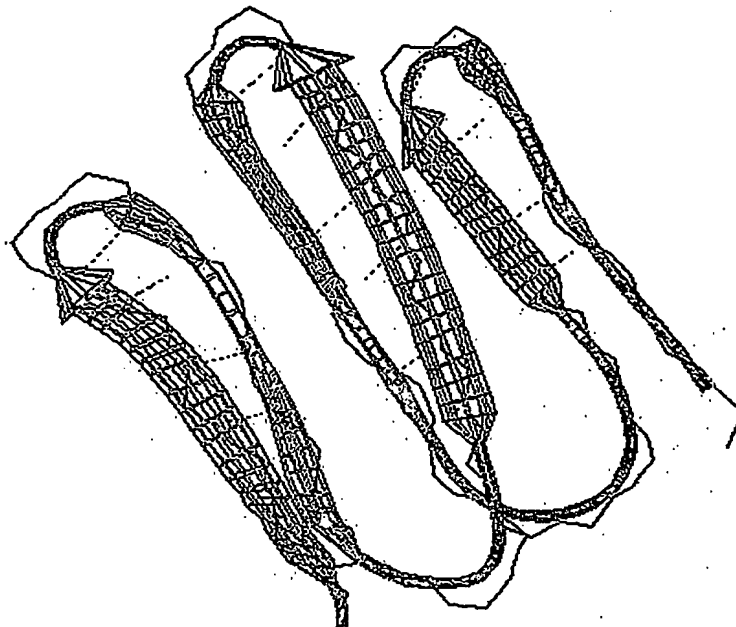
-3/5-

Consensus repeat structure of sericin precursor protein

No. of Repeats	Total Score	Length	Diagonal	BW-From	BW-To	Level
7	529.97	35	35	317	351	1
131- 164	(46.31/ 7.35)	SSSSSSTeSS...SSSR..AASSTDASNTDSNENSA				
165- 202	(82.44/20.60)	GSSTSGG..RRTYGYSSNSRDGVSSTGSSSNTDSNSNA				
203- 240	(83.27/20.91)	GSSTSGG..SSTYGYSSNSRDGVSSTGSSSNTDSNENSV				
241- 278	(68.12/15.35)	GSRRSGG..SSSHEDSSKARDENVBTGSSSNTDSNNSV				
279- 316	(82.44/20.60)	GSSTSGG..RRTYGYSSNSRDGVSSTGSSSNTDSNNSV				
317- 354	(84.15/21.23)	GSSTSGG..SSTYGYSSNSRDGVSSTGSSSNTDSNNSA				
355- 389	(83.23/20.90)	GSSTSGG..SSTYGYSSNSRDGVSSTGSSSNTDSNS				

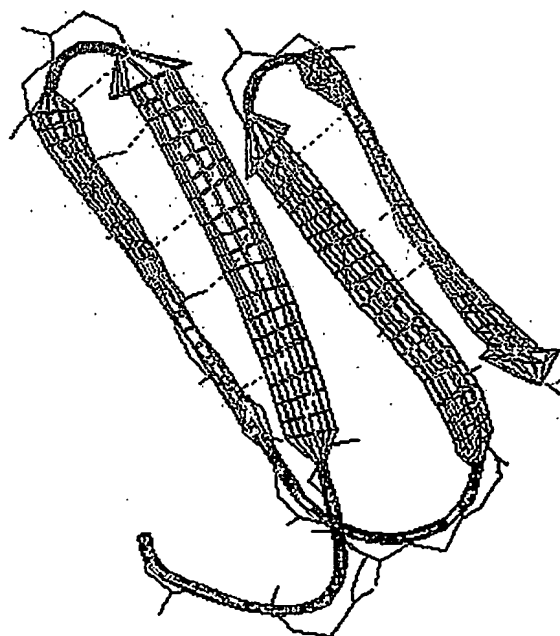
FIG. 5

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Ice nucleation protien (inaz) from the published PDB file

FIG. 6



**Swiss model for consensus sequence of sericin precursor protein using
inaz as a template**

FIG. 7

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The best LALIGN alignment of sericin precursor protein with INAC.

24.4% identity in 336 aa overlap; score: 265 E(10,000): 4.9e-16

```

      500      510      520      530      540      550
INAZ  STGTAGADSSLLIAGYGSTQTSGSESSLTAGYGSTQTAREGSTLTAGYGSTGTAGADSSLI
      : : : : : : : : : : : : : : : : : : : : : :
serici SAGAHRAKSVEQSQDKSKYTSGPEGVSTSGRSQNYKDSKQAIISGGTKSSNSNVQSDEKS
      60      70      80      90     100     110

      560      570      580      590      600      610
INAZ  AGYGSTQTSGSESSLTAGYGSTQTAQGSVLTSGYGSTQTAGAASNLTGYGSTGTAGHE
      : : : : : : : : : : : : : : : : : : : : : :
serici ASQSSSRSSQESASYSSSSSSSTEESSSSSRAASSTDASSNTDSNSNSAGSSTSGGRR
      120     130     140     150     160     170

      620      630      640      650      660      670
INAZ  SFIIAGY---GSTQTAGHKSILTAGYGSTQTARDGSDLIAGYGSTGTAGS----GSSLIA
      : : : : : : : : : : : : : : : : : : : : : :
serici TYGYSSNSRDGSVSSSTGSSSNTDSNSSNAGSSTSGGSSTYGYSSNSRDGSVSTTGSSNT
      180     190     200     210     220     230

      680      690      700      710      720      730
INAZ  GYGSTQTASYRSMILTAGYGSTQTAREHSDLVTGYGSTSTAGSNSSLIAGYGSTGTAGFKS
      : : : : : : : : : : : : : : : : : : : : : :
serici DSNNSVGSRRSGGSSSHEDSSKSRDENVTGSSSNTDSNSNSVGSSTSGGRRRTYGYSS
      240     250     260     270     280     290

```

FIG. 8